REMARKS

This amendment is submitted in response to an Office Action dated April 28, 2004. Based on this amendment, reconsideration of the merits of this patent application is respectfully requested.

In the Office Action, there were grounds of rejection applied against both of the claims in the application. Based on the changes to the claim made above, reconsideration of the merits of this patent application is respectfully requested.

The first issue in the Office Action requiring response is an objection based on sequence listing, requiring that the sequence number be inserted in the claims. Each of the claims in this application now recited the number of a sequence listing in this patent application.

Next in the Office Action were several rejections to claim 7 based on 35 U.S.C. §112, second paragraph. This rejection was for wording informalities. It is believed all of the informalities have been addressed above.

Claim 1 was rejected by the Examiner under 35 U.S.C. §112, first paragraph, for new matter. The phrase the Examiner found objectionable was "threonine residue found in the wild type sequence in the motif Val-Asn-Phe-Thr." The amino acid sequence is found in the sequence listing as filed, at residues 336 to 340. The word "wild-type" is used in the specification in paragraphs 17 and 34. Accordingly, the applicants took the Examiner's objection to be to the word "motif." That word has been replaced above with the term "amino acid sequence," which could hardly be objectionable.

Lastly, claim 7 was rejected under 35 U.S.C. §102 over the sequence disclosed in the Frandsen paper. As the applicants explained in the last response, the sequence presented by Frandsen seems to be a variation on the sequence of Skadsen, or is perhaps the same sequence with one or both of the sequences having a few errors, as is common in the art. Those differences result in the Frandsen sequence having a few more amino acids. The aspartate residue which is at position 105 in the Skadsen sequence, and in SEQ ID NO:1 here, appears at residue 110 in the Frandsen sequence.

Those of skill in the art recognize today, and recognized at the time of filing this patent application, that the amino acid sequences of proteins are compared by "best-fit" analysis that matches amino acid sequences of similar proteins as best possible. The applicants used a "best-fit" analysis to compare the sequences of various α-glucosidase proteins in paragraph 13 of the specification and in Fig. 2. Hence there is antecedent basis in the specification for the use of "best-fit" as a method of protein comparison. It is believed

that this language is definite and is appropriate given the usage by those of ordinary skill in the art. This language also distinguishes the claim from Frandsen. In the Frandsen sequence, the amino acid that corresponds is the aspartate at position 110. We know this since Frandsen also does a best-fit sequence comparison, with the sequence (GenBank U22450), that is SEQ ID NO:1, and illustrates in Fig. 6 that residue 110 of his sequence aligns with residue 105 of the prior sequence (SEQ ID NO:1). This same analysis is true for the aspartate residues at position 508, which corresponds to the aspartate located at 511 in the Fradsen sequence in Fig. 6 of the paper. Thus the Frandsen sequence has not modified the native aspartate residues at the locations claimed here, and the reference does not anticipate the claims of this invention.

Based on the foregoing, a reconsideration of this patent application and an early and favorable reply on the merits is respectfully requested.

Respectfully submitted,

Nicholas J. Seay
Reg. No.: 27,386
Attorney for Applicants
QUARLES & BRADY LLP
P.O. Box 2113
Madison, WI 53701

TEL 608/251-5000
FAX 608/251-9166